

01/11

APPENDIX C FIG 1
DRAFTSMAN

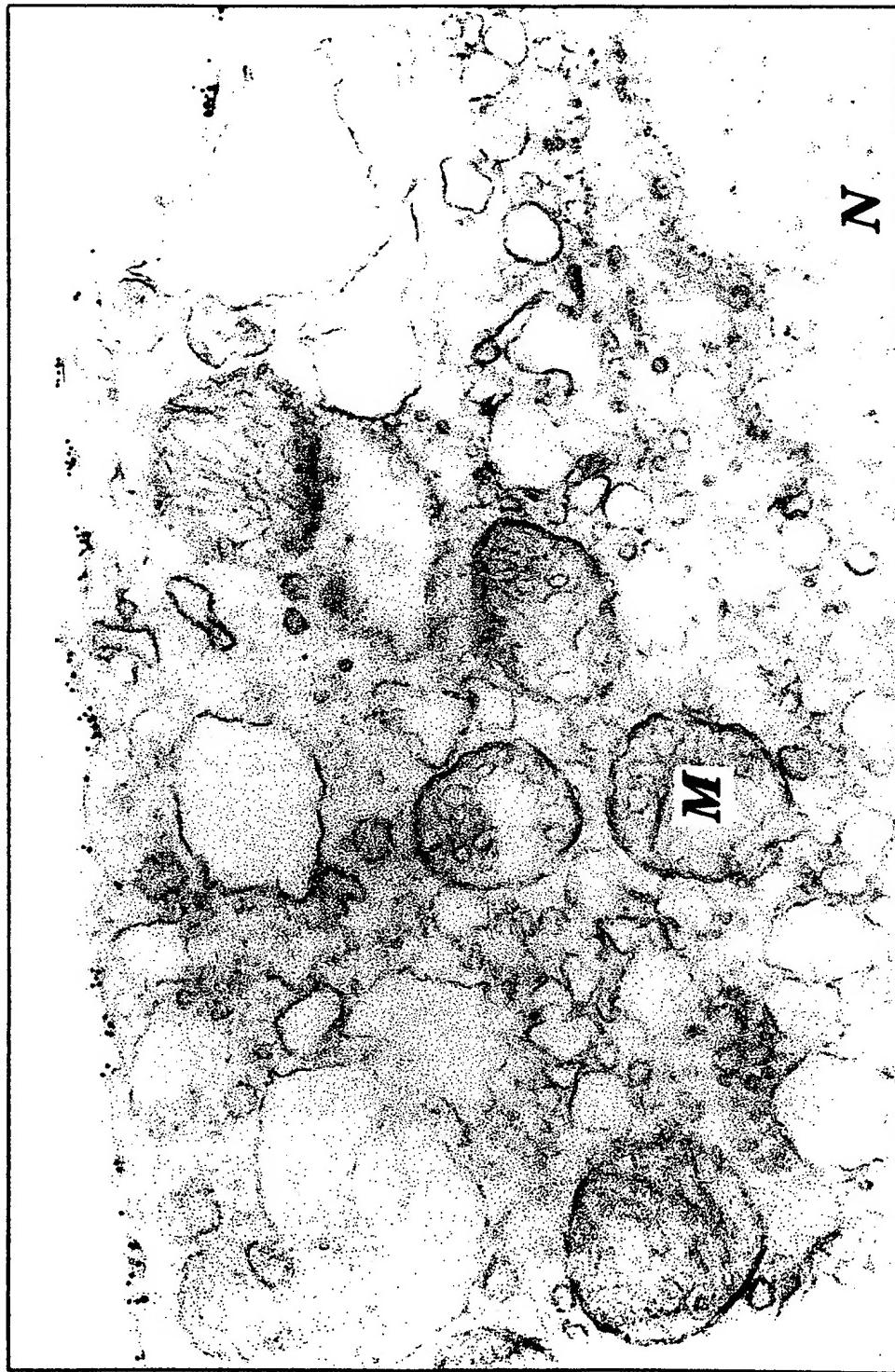


FIG. 1

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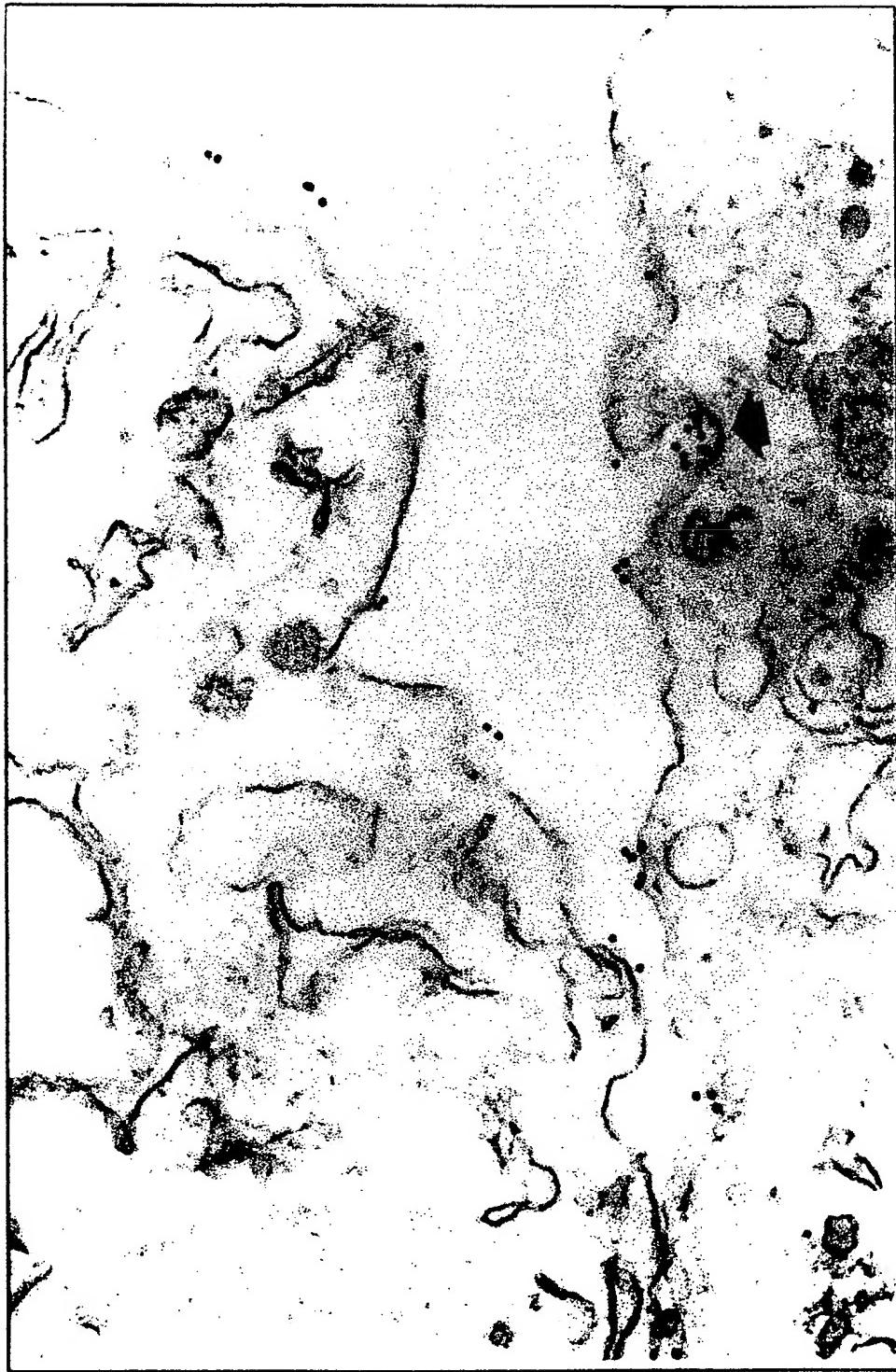
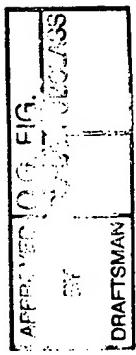


FIG. 2

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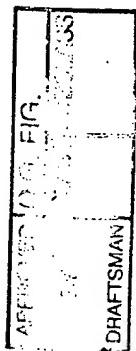


FIG. 3

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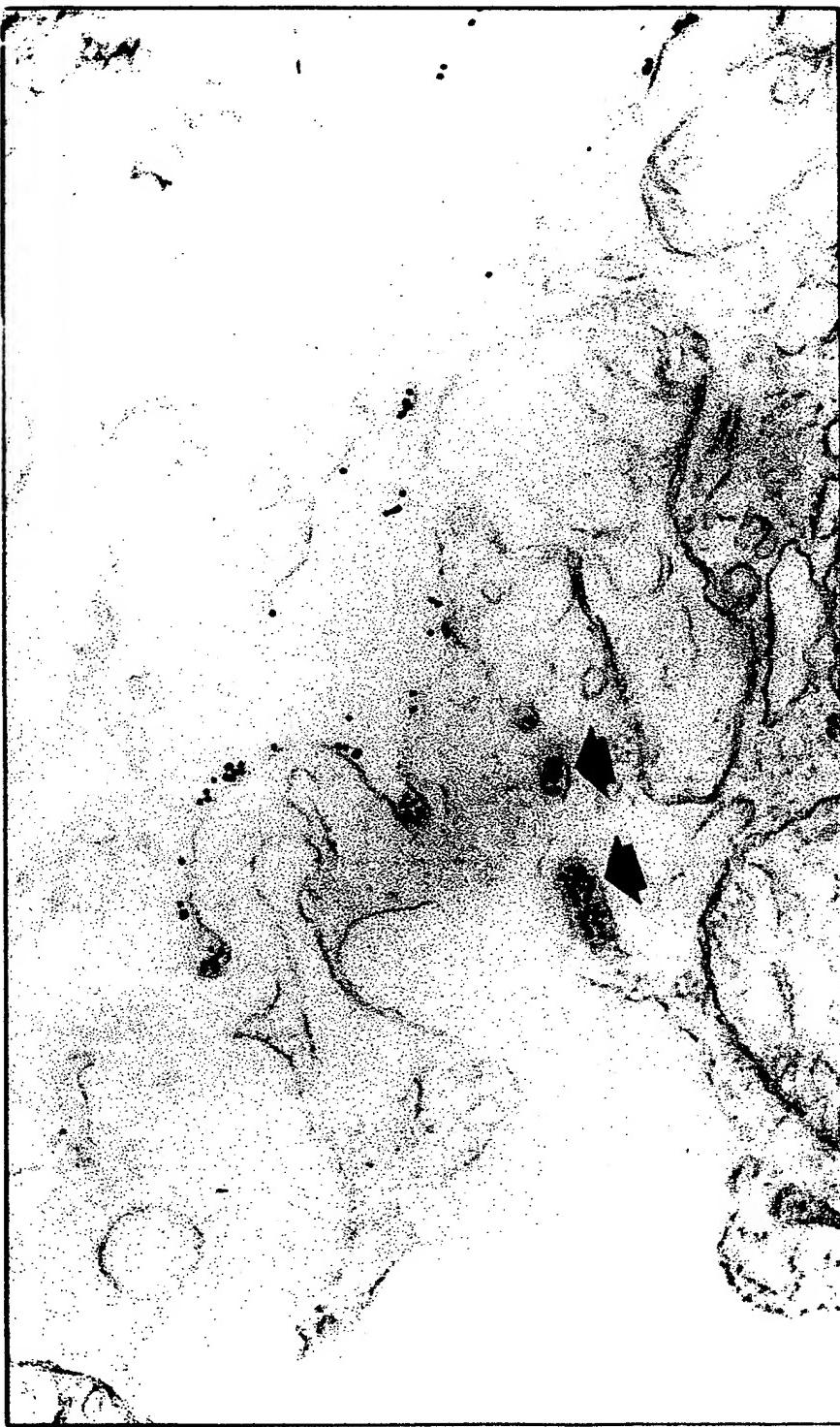


FIG. 4

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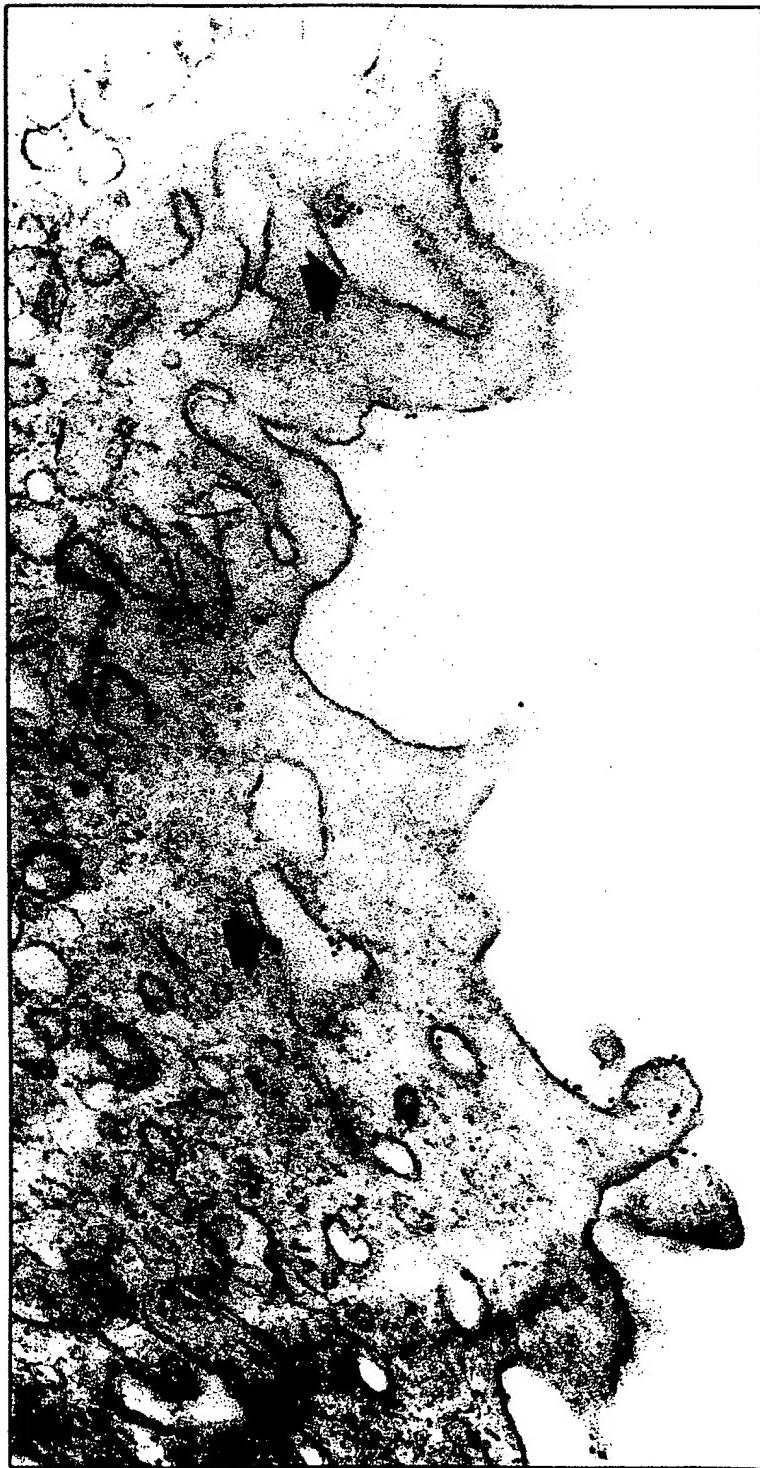


FIG. 5

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APPROVED	O. G. FIG.
SPEC.	CLASS
SPEC.	SUBCLASS
DRAFTSMAN	

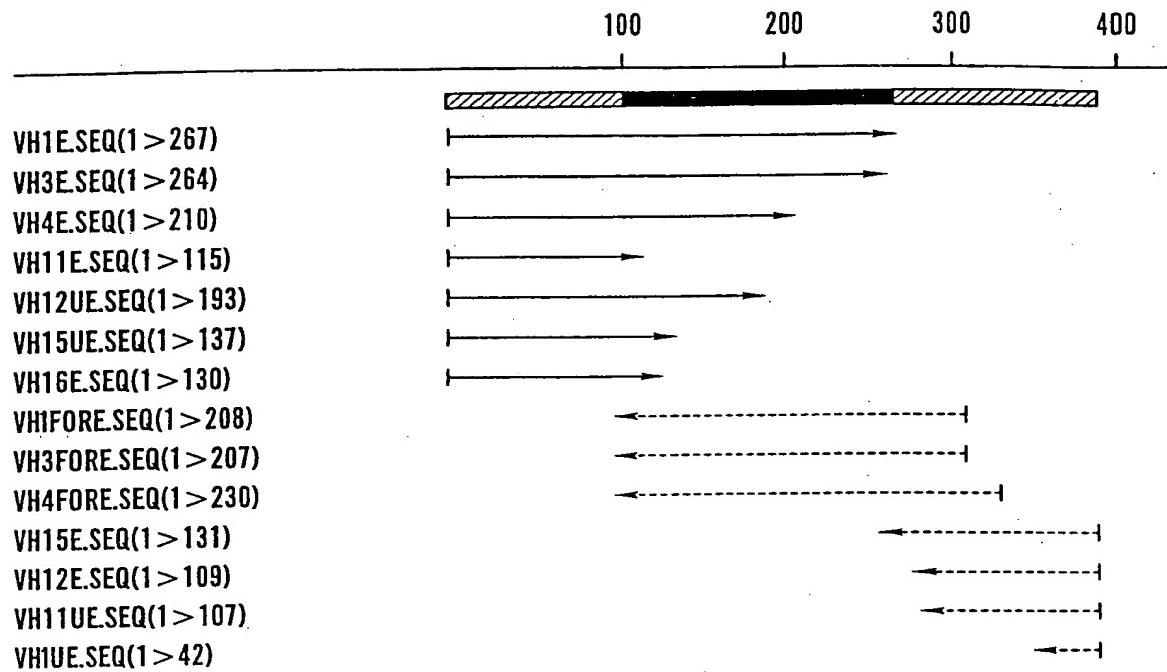


FIG. 6

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ENZYMES: ALL 74 ENZYMES (NO FILTER)

SETTINGS: LINEAR, CERTAIN SITES ONLY, STANDARD GENETIC CODE

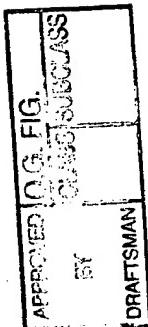


FIG. 7

<p>SEQ. ID. NO. 1 TCTCCIGTCAGGAACCTGAGGTCCTCTCTGAGGTCCAGCTGAAACAGCTCTGGACCTGAACTGGTGAAG SEQ. ID. NO. 2 AGAGGACAGTCCTTGAGCTCCACAGGAGAGACTCCAGGTGAGGTGTCAGACCTGGACTTGACCACTTC SEQ. ID. NO. 3 S P V R N C R C P L . G P A A T V W T . T G E SEQ. ID. NO. 4 L L S G T A G V L S E V Q L Q Q S G P E L V K SEQ. ID. NO. 5 L S C Q E L Q V S S L R S S C N S L D L N W . S</p>	
<p>SEQ. ID. NO. 1 CCTGGGACTTCAGTGAGGATATCTGCAAGACTCTGGATAACACATTCACTGAATATACCATACACTGGG SEQ. ID. NO. 2 GGACCCCTGAAGTCACCTCCATAGGACGTTCTGAAGACCTATGTTAAGTGACTTATATGGTATGIGACCC SEQ. ID. NO. 3 A W D F S E D I L Q D F W I H I H . I Y H T L G SEQ. ID. NO. 4 P G T S V R I S C K T S G Y T F T E Y T I H W SEQ. ID. NO. 5 L G L Q . G Y P A R L L D T H S L N T P Y T G</p>	
<p>SEQ. ID. NO. 1 TGAACCAGAGCCATGAAAGAGCCTTGAGTGGATTGAAACATCAAATCTAACATGGTGGTACCCCTA SEQ. ID. NO. 2 ACTTGGCTCGGTAACCTTCTCGGAACTCACCTAACCTTGTAGTTAGGATTGTTACCACTGGTGGAT SEQ. ID. NO. 3 E A E P W K E P . V D W K H Q S . Q W W Y H L SEQ. ID. NO. 4 V K Q S H G K S L E W I G N I N P N N G G T T Y SEQ. ID. NO. 5 S R A M E R A L S G L E T S I L T M V V P P</p>	
<p>SEQ. ID. NO. 1 CAATCAGAAGTTCGAGGACAAGGCCACATTGACTGTAGACAAGTCCTCCAGTACAGCCTACATGGAGCTC SEQ. ID. NO. 2 GTTAGTCCTCAAGCTCCGTGTCGGTGTAACTGACATCTGTCAGGAGTCATGTCGGATGTACCTGGAG SEQ. ID. NO. 3 Q S E V R G Q G H I D C R Q V L Q Y S L H G A SEQ. ID. NO. 4 N Q K F E D K A T L T V D K S S S T A Y M E L SEQ. ID. NO. 5 T I R S S R T R P H . L . T S P P V Q P T W S S</p>	
<p>SEQ. ID. NO. 1 CGCAGCTAACATCTGAGGATTCTGAGCTCTATTATGGCAGCTGGTGGAACTTTGACTACTGGGGCC SEQ. ID. NO. 2 GCGTGGATTGTAGACTCTAACAGACCTCAGATAATAACACGTCGACCAACCTTGAAACTGATGACCCCG SEQ. ID. NO. 3 P Q P N I . G F C S L L L C S W L E L . L L G P SEQ. ID. NO. 4 R S L T S E D S A V Y Y C A A G W N F D Y W G SEQ. ID. NO. 5 A A . H L R I L Q S I I V Q L V G T L T T G A</p>	
<p>SEQ. ID. NO. 1 AAGGCACCACTCTCACAGTCCTCAGCCAAAAGACACCC SEQ. ID. NO. 2 TTCCGTGGTGAGAGTGTCAGAGGAGTCGGTTTGCTGTGGG SEQ. ID. NO. 3 R H H S H S L L S Q N D T SEQ. ID. NO. 4 Q G T T L T V S S A K T T P SEQ. ID. NO. 5 K A P L S Q S P Q P K R H P</p>	

FIG. 7

TREATMENT AND DIAGNOSIS OF PROSTATE CANCER

INV: N. BANDER

SN: 09/357,704

08/11

APPROVED	O. G. FIG.
CLASS	100 SUBCLASS
BY	
DRAFTSMAN	

LIPMAN-PEARSON PROTEIN ALIGNMENT
 KTUPLE: 2; GAP PENALTY: 4; GAP LENGTH PENALTY: 12

SEQ1(1>115) J591VH.PRO (1>115)	SEQ2(1>125) MUVHIIA.PRO (1>125)	SIMILARITY INDEX	GAP NUMBER	GAP LENGTH	CONSENSUS LENGTH
		75.6	2	10	125

The diagram shows two protein sequences aligned vertically. Arrows above the sequences indicate matching positions. Gaps are represented by dashes. The top sequence starts with 'EVOLQOQSGPEL' and ends with 'INPGNGTS'. The bottom sequence starts with 'YNQKFEDKATLTVDKSSSTAYMELRSLTSEDSAVYYCAAG' and ends with 'AFDYWGQGTT'. Arrows point from positions 10, 20, 30, 40, and 50 in the top sequence to corresponding positions in the bottom sequence. Other arrows point from positions 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, and 120 in the bottom sequence back to the top sequence, indicating matches.

LTVSS
 :TVSS
 VTVSS

FIG. 8

TREATMENT AND DIAGNOSIS OF PROSTATE CANCER

INV: N. BANDER

SN: 09/357,704

09/11

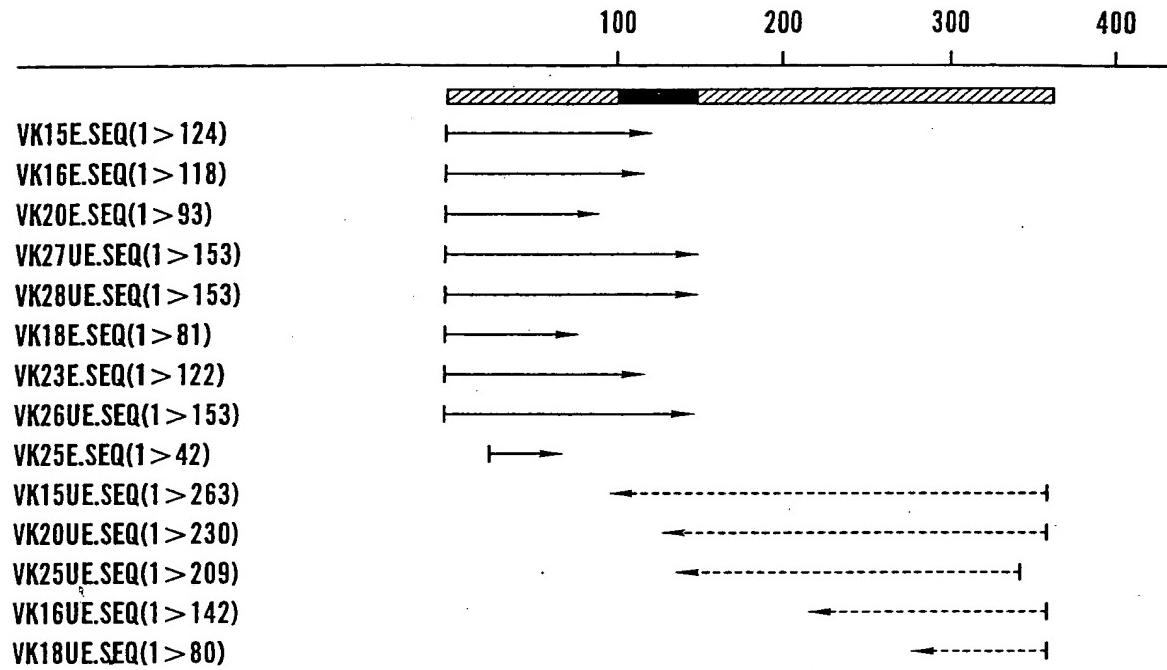
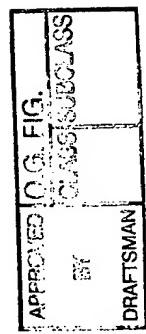


FIG. 9

TREATMENT AND DIAGNOSIS OF PROSTATE CANCER

INV: N. BANDER

SN: 09/357,704

10/11



ENZYMES: ALL 74 ENZYMES (NO FILTER)
 SETTINGS: LINEAR, CERTAIN SITES ONLY, STANDARD GENETIC CODE

Alu | Hph I
 SEQ. ID. NO. 9 T T A T A T G G A G C T G A T G G G A A C A T T G T A A T G A C C C A A T C T C C C A A T C C A T G T C C A T G T C A G T A G G G A G A G 70
 SEQ. ID. NO. 10 A A T A T A C C T O G A C T A C C C T T G T A A C A T T A C T G G G T T A G A G G G T T A G G T A C A G G T A C A G T C A T C C T C T C T
 SEQ. ID. NO. 11 L Y G A D G N I V M T Q S P K S M S M S V G E
 SEQ. ID. NO. 12 Y M E L M G T L . . P N L P N P C P C Q . E R
 SEQ. ID. NO. 13 I I W S . . W E H C N D P I S Q I H V H V H V S R R E
 Hae III | Bsr I
 SEQ. ID. NO. 9 G G G T C A C C T T G A C C T G C A A G G C C A G T G A G A A T G T G G T T A C T T A G T T C C T G G T A C A C A G A A A C C A G A 140
 SEQ. ID. NO. 10 O C C A G T G G A C T G G A O G T C C C G T C A C T C T T A C A C C A A T G A A T A C A A A G G A C C A T A G T G T C T T T G G T C T
 SEQ. ID. NO. 11 R V T L T C K A S E N V V T Y V S W Y Q Q K P E
 SEQ. ID. NO. 12 G S P . P A R P V R M W L L M F P G I N R N Q
 SEQ. ID. NO. 13 G H L D L Q G Q . E C G Y L C F L V S T E T R
 Alw26 I | Fok I | Hpa II | Rsa I | Ava II | Mbo I | Bsr I | Sau96 I | Dpn I | Bsa0 I | Pvu I
 SEQ. ID. NO. 9 G C A G T C T C C T T A A A C T G C T G A T A T A C G G G C A T C C A A C C G G T A C A C T G G G T T C C C C G A T G C T C A C A G G C 210
 SEQ. ID. NO. 10 C G T C A G A G G A T T T G A C G A C T A T A T G C C C C G T A G G T T G G C C A T G T G A C C C C A G G G G C T A G C G A A G T G T C C G
 SEQ. ID. NO. 11 Q S P K L L I Y G A S N R Y T G V P D R F T G
 SEQ. ID. NO. 12 S S L L N C . Y T G H P T G T L G S P I A S Q A
 SEQ. ID. NO. 13 A V S . T A D I R G I Q P V H W G P R S L H R
 Mbo I | Dpn I | Bsp6 II | Mbo II | Ec057 I
 SEQ. ID. NO. 9 A G T G G A T C T G C A A C A G A T T T C A C T C T G A C C A T C A G C A G T G T G C A G G G T G A A G A C C T T G C A G A T T A T C A T T 280
 SEQ. ID. NO. 10 T C A C C T A G A C G T G T C T A A A G T G A G A C T G G T A G T C G T C A C A C G T C O G A C T T C T G G A A C G T C T A A T A G T G A
 SEQ. ID. NO. 11 S G S A T D F T L T I S S V Q A E D L A D Y H
 SEQ. ID. NO. 12 V D L Q Q I S L . P S A V C R L K T L Q I I T
 SEQ. ID. NO. 13 Q W I C N R F H S D H Q Q C A G . R P C R L S L
 Alu I | Rsa I | Ava II | Sau96 I | Alu I
 SEQ. ID. NO. 9 G T G G A C A C G G T T A C A G C T A T C C G T A C A C G T T C G G A G G G G G A C C A A G C T G G A A A T A A A A C G G G C T G A T G C 350
 SEQ. ID. NO. 10 C A C C T G T C C C A A T G T G O G A T A G G C A T G T G C A A G C C T C C C C C C T G G T T C G A C C T T A T T T G C C C G A C T A G G
 SEQ. ID. NO. 11 C G Q G Y S Y P Y T F G G G T K L E I K R A D A
 SEQ. ID. NO. 12 V D R V T A I R T R S E G G P S W K . N G L M
 SEQ. ID. NO. 13 W T G L Q L S V H V R R G D Q A G N K T G . . C
 SEQ. ID. NO. 9 T G C A C C A A C T G T A → 363
 SEQ. ID. NO. 10 A C G T G G G T T G A C A T
 SEQ. ID. NO. 11 A P T V
 SEQ. ID. NO. 12 L H Q L Y
 SEQ. ID. NO. 13 C T N C →

FIG. 10

TREATMENT AND DIAGNOSIS OF PROSTATE CANCER

INV: N. BANDER

SN: 09/357,704

11/11

APPROVED	C. S. FIG.
BY	DR. JOHN B. BANDER
DRAFTSMAN	

LIPMAN-PEARSON PROTEIN ALIGNMENT
 KTUPLE: 2; GAP PENALTY: 4; GAP LENGTH PENALTY: 12

SEQ1(1>107) J591VK.PRO (1>107)	SEQ2(1> 1 1 1) MUVKV.PRO (1>109)	SIMILARITY INDEX 60.4	GAP NUMBER 2	GAP LENGTH 2	CONSENSUS LENGTH 109
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The diagram shows two protein sequences aligned vertically. Above each sequence are numbered arrows pointing to specific amino acid positions. The top sequence is J591VK.PRO and the bottom sequence is MUVKV.PRO. The arrows indicate matches between positions 10, 20, 30, 40, and 50. Below these, the top sequence has arrows at 60, 70, 80, 90, and 100, while the bottom sequence has arrows at 70, 80, 90, and 100. The sequences themselves are as follows:

Top Sequence (J591VK.PRO):
 NIVMTQSPKMSMSVGERVLTCKAS-ENVVTYVSWYQQKPEQSPKLLIYASNRYTGVP
 : I MTQSP.S:S S:G:RVT:TC:AS :: .Y.:WYQQKP. SPKLLIY AS. .:GVP
 DIQMTQSPSSILSASLGDRTITCRASODDISNYLNWYQQKPGGSPKLLIYYASRLHSGVP

Bottom Sequence (MUVKV.PRO):
 DRFTIGSGSATDFTLTISSVQAEDLADYHCGQGYSY-PYTFGGGTKEIK
 .RF:GSGS:TD:LTIS:::ED:A.Y C QG : P TFGGGTKEIK
 SRFSGSGSGTDYSLTISNLQEDIATYFOQQQNTLPPRTFGGGTKEIK

FIG. 11